Please replace paragraphs 0039, 0040 and 0041 with the following rewritten paragraphs, respectively:

Figure 13 (SEQ ID NOS 34-42, respectively, in order of appearance) illustrates a first peptide sequence pileup of HAL from various bacteria, including *Corynebacteriaceae, B. subtilis*, *S. griseus*, *P. putida*.

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Figure 14 (SEQ ID NOS 43-64, respectively, in order of appearance) is a second peptide sequence pileup of HAL from various bacteria, including *Corynebacteriaceae, S. griseus*, and *D. radiodurans*

Figure 15 (SEQ ID NOS 65-66, respectively, in order of appearance) is a comparison between the amino acid sequence of *S. griseus* ("STRG") and *Corynebacteriaceae* ("HAL"); positions of an amino acid identity are delineated by "*".

Please replace paragraph 00127 with the following rewritten paragraph:

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Two of the resulting probes (TM63 and TM74), shown in Table 1, below, were labeled, mixed, and used to screen the above genomic library. Oligos were labeled with γ^{32}PATP using T4 polynucleotide kinase as described (Ausubel, *et al*, eds, 1994. "Current Protocols in Molecular Biology," John Wiley and Sons, Inc.,) and cleaned up using Elutips (Schleicher & Schuell). Hybridization of duplicate filters was carried out in a Bellco hybridization oven at 37°C using the SSPE protocol as described (Ausubel, *et al.*, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994). Filters were washed in 6X SSC with 0.5%SDS (Ausubel, *et al*, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994) at 37°C. Filters were then washed at successively higher temperatures in 3 M TMAC (Ausubel, *et al*, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994) until very little radioactivity could be detected with a survey meter (generally 45 - 55°C). Upon exposure to X-Ray film (Kodak X-Omat), colonies which were evident on both replicate filters were picked with a wooden toothpick and

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transferred to a fresh nylon filter overlaid onto an LB/ampicillin plate. This procedure was repeated until a homogeneous population was achieved.

Table 1: oligonucleotides (SEQ ID NOS 1-27, respectively, in order of appearance) with DNA sequence and approximate coordinates relative to the ATG start codon.

Name	Length	Sequence (5' to 3')	Coordinates
TM63	30	CGCGTTCAGGACGCATACTCCGTTCGCTGC	838-867
TM74	24	GCCCATGGAAACGTGGTCTTCCTG	1370 - 1393
TM85	21	ATCATCATGCCCGAGTCCACA	1156 - 1176
TM87	21	GCCATCAGGAAGACCACGTTT	990 - 971
TM89	20	ATGCAGGAAGACCACGTTTC	1246 - 1265
TM91	21	ATCGAGGTCCGCCAATGCCAT	648 - 628
TM92	18	ACCGGAGCAGCCCAGTGA	441 - 424
TM93	20	TGCTTGAAGTATTGCGCCAG	1403 - 1422
TM94	18	GATCCTCGGGTGCGATGT	226 - 209
TM95	18	ATGCTGATCGGGCTTCGT	92 - 74
TM96	27	ATTTGATTCATATGGCTTCCGCTCCTC	-11 - +16
TM97	28	ATCTTGGATCCGAACATGGTGCGTTGCA	Beyond C-Terminus
TM98	18	AGCACCAGAT CGATGCAC	128 - 145
TM99	18	TGGCATGGGTGAACCGGT	267 - 284
TM101	18	ATCAGCGTTGAAGCCCAG	682 – 699
TM103	18	ACGTGCTGGACTTCCTTG	1019 - 1036
TM105	18	GTGCATAAGGCCCTCGAA	1501 - 1518